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Figure 1. The *CaESS1* gene of *Candida albicans*.

1 GATCAACCAATAGATGTTGTTGCTAACCAAGTCAAAGACGCGTTGAAGACAAGAGGTATTTAGACACACAAGCATTAGTCACTTGAAT 88  
 89 ACATATACACTTGACATTCTCTTCCAATACATATTAACCTACTGTACATTTACCAAAACTTCTCTCTTTTCTATATTCTTCATCAACACAAGATTTTC 180  
 189 GTTCTTGGCTTTTGTGTTGTTATTTGTCATCAGTTTAGCTTGAATTTTGTGAGTATATATCATC ATG GCA TCG ACA TCA ACA GGC TTA 279  
 1 M A S T S T G L B  
 280 CCA CCT AAT TGG ACG ATT AGA GTA TCC AGA TCC CAT AAC AAA CAG TAT TTC TTA AAC CAA TCT ACC AAT GAG TCG 354  
 9 P P N W T I R V S R S H N K E Y F L N Q S T N E S  
 355 TCT TGG GAC CCA CCT TAT GGC ACT GAC AAA GAA GTA TTG AAT GCA TAC ATT GCG AAG TTT AAA AAC AAT GGT TAC 429  
 34 S W D P P Y G T D K E V L N A Y I A K F K N N G Y  
 430 AAC CCA CTT CTC AAT GAG GAT GGC CAG GTT ACA GTT TCT CAT TTG TTG ATC AAG AAC AAT CAA TCA AGA AAA CCC 504  
 59 K P L V N E D G Q V R V S H L I I K N N Q S R K P  
 505 AAG TCT TGG AAG TCC CCA GAT GGT ATA AGT AGA ACT AGA GAC GAA TCT ATA CAG ATA TTG AAG AAA CAT TTG GAA 579  
 84 K S W K S P D C I S R T R D E S I Q I L K K H L E  
 580 AGA ATA TTG AGT GGT GAG GTT AAA CTA AGT GAA TTG GCA AAT ACC GAA AGT GAT TCC AGC TCA CAT GAC AGA GGT 654  
 109 R I L S G E V K L S E L A N T R S D C S S H D R C  
 655 GGT GAT TTA GGG TTT TTT AGC AAA GGA CAA ATG CAA CCA CCA TTG GAA GAA GCG GCA TTC AAT TTG CAT CTT GGA 729  
 134 C D L G F F S K C Q M Q P P F E E A A F N L H V G  
 730 GAA GTC AGT AAC ATA ATT GAA ACC AAT AGT GGT GTC CAT ATC CTC CAA AGA ACA GGA TAA ATCAAGATATTGGAATTGCA 809  
 159 E V S N I I E T N S G V H I L Q R T G  
 810 TGAAAAATGAAAATAAATAGAGACAAGTCTATAGATTTGCTAACCAAAAAAGCGATGGCTCACAAAAGTCGAAAACGTGTGGAGACAACATCTTACCAGG 909  
 910 TACACGGCOATTAATACTCTAATCGTCCGATATTTATATAATCGGAACGTTTCCCGTCATTGGTTTGTATATTTCGATCC 989

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Figure 1. Complete nucleotide sequence of the *CaESS1* gene from *Candida albicans* and its predicted translation product. The *CaESS1*-encoded protein is 177 amino acids long and has a predicted MW of 19.8 Kd. It is 42% identical to the *ESS1* protein of *Saccharomyces cerevisiae*.

Figure 1B. Gene Knockout of *CaESS1* in *Candida albicans*.

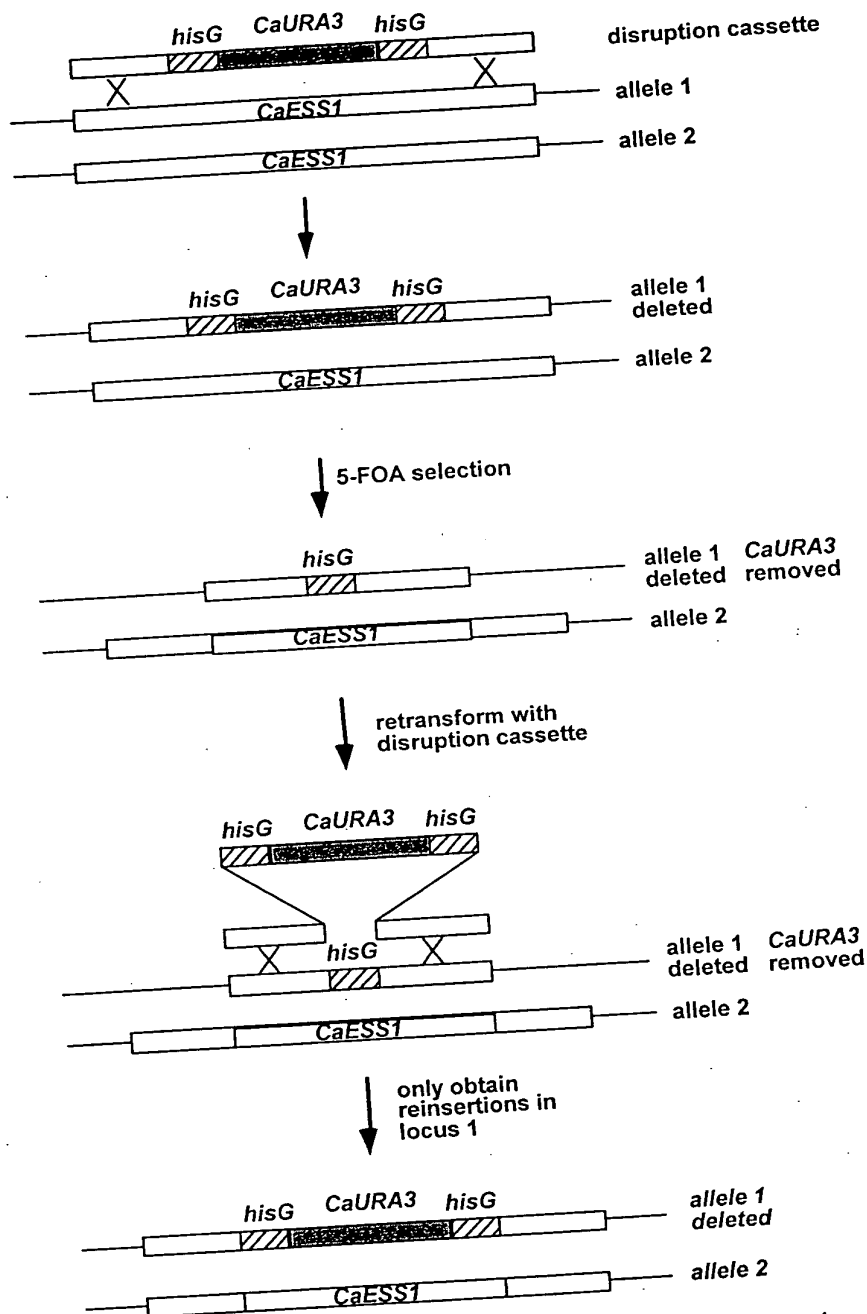
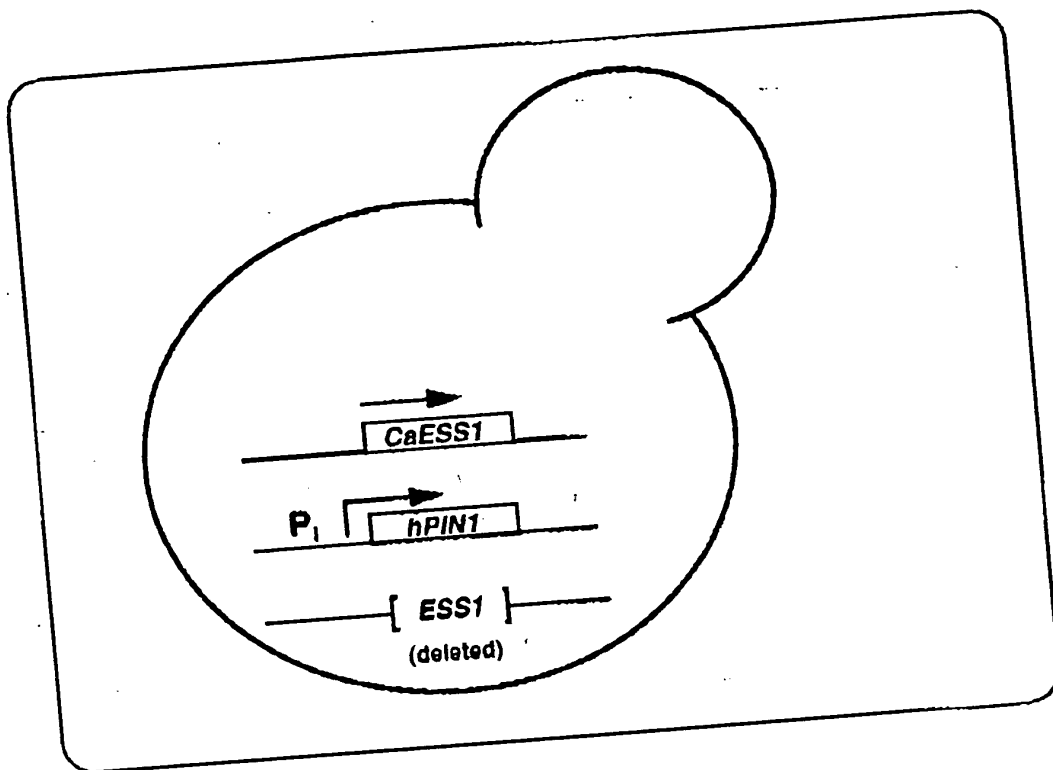


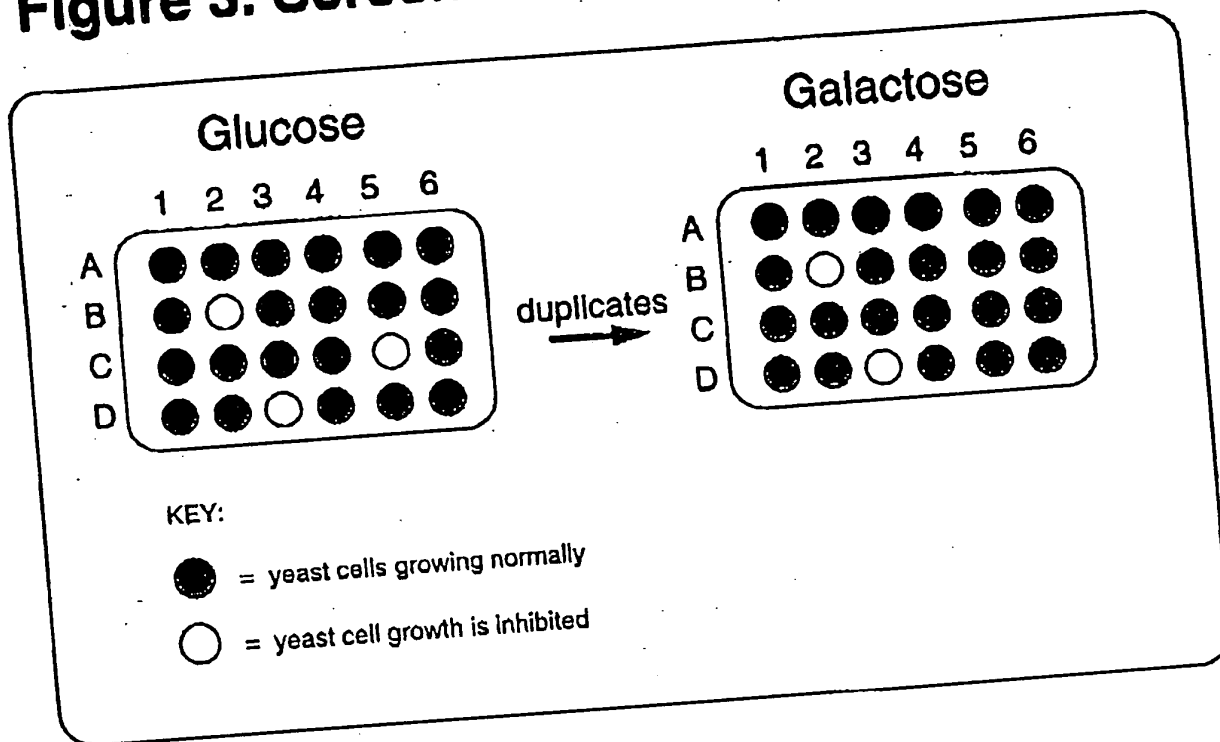
Figure 1B. *CaEss1* was deleted in strain CAI4 by the method of Fonzi and Irwin (1993). *Ura*<sup>+</sup> transformants were selected, genomic DNA was prepared and analyzed by Southern hybridization and by PCR. Results confirmed homologous recombination and gene deletion of the first allele as outlined in the figure. The *CaURA3* gene was then removed by selection with 5-FOA, and diploid disruption strains (*caess1/CaESS1*) were used for retransformation with the *hisG-CaURA3-hisG* disruption cassette as before. No homozygous deletion strains (*caess1/caess1*) were obtained (see Table 1). Instead the *hisG-CaURA3-hisG* cassette reinserted into the already disrupted allele in all *Ura*<sup>+</sup> transformants analyzed.

**Figure 2. Yeast Strain to Identify Inhibitors  
Specific for *Candida albicans* CaESS1**



008720-2420580

**Figure 3. Screen for *CaESS1* Inhibitors**



## Figure 4. Screen for *hPIN1* Inhibitors

